

430 CAGGTGCTGGAGGACATCACTGTCAGACACAAAGCCCGCGACATCCCTCAGGGCTCC 489

161 LeuAlaTyLeuGluGlnAlaSerAlaAsnIleProAlaProLeuLysProThr 178

490 TTGGCCTACCTGGAGCAGGCATCTGCCAACATCCCTGCACCTCTGAAGCCAACG 543

RESULT 3

AX017517

LOCUS AX017517 1071 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 65 from Patent WO9947655.

ACCESSION AX017517

VERSION AX017517.1 GI:10042314

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C. Human nucleic acid sequences from normal breast tissue Patent: WO 9947655-A 65 23-SEP-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)

AUTHORS

TITLE Human nucleic acid sequences from normal breast tissue

JOURNAL

COMMENT

FEATURES

source

1. .1071

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 281 a 218 c 255 g 317 t

ORIGIN

Alignment Scores:

Pred. No.: 1,24e-68 Length: 1071

Score: 918.00 Matches: 178

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-137-2 (1-178) x AX017517 (1-1071)

Qy 1 MetAlaAlaProLeuGlyGlyMetPheSerGlyGlnProProGlyProGlnAlaPro 20

Db 10 ATGGCGGCTCCACTAGGGGTATGTTTCTGGGACACCCGGTCCCGCTCAGGCCCCG 69

Qy 21 ProGlyLeuProGlyGlnAlaSerLeuGlnAlaProGlyAlaProArgProSer 40

Db 70 CCGGGCTTCGGGCGCCAGCTTCCTTCAGGACGCTCCAGGCGCTCCTAGACCTTCC 129

Qy 41 SerSerThrLeuValAspGluLeuGluSerSerPheGluAlaCysPheAlaSerLeuVal 60

Db 130 AGCAGTACTTTGGTGGACGATGGAGTTCATCTTCGAGGCTTGTTCGATCTCTGGTG 189

Qy 61 SerGlnAspTyrValAsnGlyThrAspGlnGluGluLeuLeuThrGlyValAsnGlnCys 80

Db 190 AGTCAGACATATGTCATGGCCACCGATCAGAGAGAAATTCGACCGGTGTTCAGTGT 249

Qy 81 IleGlnLysPheLeuAspIleAlaArgGlnThrGluCysPhePheLeuGlnLysArgLeu 100

Db 250 ATCCAGAAGTTTCTGGATATTGACAGACACAGAGATGTTTCTTACAAAGAAATG 309

Qy 101 GlnLeuSerValGlnLysProGluGlnValIleLysGluAspValSerGluLeuArgAsn 120

Db 310 CAGTTATCTGTCCAGAAACCCAGAGCAAGTATTCAGAGAGATGTTTCAGACTAAGGAAT 369

Qy 121 GluLeuGlnArgLysAspAlaLeuValGlnLysHisLeuThrLysLeuArgHisTrpGln 140

Db 370 GAATTACAGCGGAAGATGCACTAGTCCAGAGCACTTGACAAAGCTGAGGCATTCGAC 429

Qy 141 GlnValLeuGluAspIleAsnValGlnHisLysLysLysProAlaAspIleProGlnGlySer 160

430 CAGGTGCTGGAGGACATCACTGTCAGACACAAAGCCCGCGACATCCCTCAGGGCTCC 489

161 LeuAlaTyLeuGluGlnAlaSerAlaAsnIleProAlaProLeuLysProThr 178

490 TTGGCCTACCTGGAGCAGGCATCTGCCAACATCCCTGCACCTCTGAAGCCAACG 543

RESULT 4

BD135207

LOCUS BD135207 1071 bp DNA linear PAT 18-SEP-2002

DEFINITION Human nucleic acid sequence originating in normal mammary tissue.

ACCESSION BD135207

VERSION BD135207.1 GI:23230152

KEYWORDS JP 2002506639-A/54.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Speft,T., Hintzman,B., Shcmitt,A., Pirarski,C., Duhl,E. and Rosenthal,A. Human nucleic acid sequence originating in normal mammary tissue Patent: JP 2002506639-A 54 05-MAR-2002; METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH

AUTHORS

TITLE Human nucleic acid sequence originating in normal mammary tissue

JOURNAL

COMMENT

OS Homo sapiens (human)

PN JP 2002506639-A/54

PD 05-MAR-2002

PF 19-MAR-1999 JP 2000536838

PR 20-MAR-1998 DE 198 13 835.0

PI THOMAS SPEFT, BERND HINTZMAN, ARMIN SHCMITT, CHRISTIAN PIRARSKI, PI EDGAR DUHL,

P1 ANDRE ROSENTHAL

PC C12N15/09, A61K48/00, A61P35/00, A61P43/00, A61P43/00, C07K14/47, C07K16/18

PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//A61K38/00, PC C12N15/00,

CC C12N5/00, A61K37/02

CC Human nucleic acid sequence originating in normal mammary CC

FH Key

FT source

PT Location/Qualifiers

1. .1071

/organism="Homo sapiens (human)"

Location/Qualifiers

1. .1071

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 281 a 218 c 255 g 317 t

ORIGIN

Alignment Scores:

Pred. No.: 1,24e-68 Length: 1071

Score: 918.00 Matches: 178

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-137-2 (1-178) x BD135207 (1-1071)

Qy 1 MetAlaAlaProLeuGlyGlyMetPheSerGlyGlnProProGlyProGlnAlaPro 20

Db 10 ATGGCGGCTCCACTAGGGGTATGTTTCTGGGACACCCGGTCCCGCTCAGGCCCCG 69

Qy 21 ProGlyLeuProGlyGlnAlaSerLeuGlnAlaProGlyAlaProArgProSer 40

Db 70 CCGGGCTTCGGGCGCCAGCTTCCTTCAGGACGCTCCAGGCGCTCCTAGACCTTCC 129

Qy 41 SerSerThrLeuValAspGluLeuGluSerSerPheGluAlaCysPheAlaSerLeuVal 60

Db 130 AGCAGTACTTTGGTGGACGATGGAGTTCATCTTCGAGGCTTGTTCGATCTCTGGTG 189

Qy 61 SerGlnAspTyrValAsnGlyThrAspGlnGluGluLeuLeuThrGlyValAsnGlnCys 80

485 GCTCTTGGCTACCTGGAGCAGGATCTGCCAATCTCCTGCACCTCTGAAGCAACGT 544  
 541 GAGCAAGGGCAGAGGAGTTGGCCCTATGAGTGGGCTGATGCTGAGGTGGCCACACAT 600  
 545 GAGCAAGGGCAGAGGAGTTGGCCCTATGAGTGGGCTGATGCTGAGGTGGCCACACAT 604  
 601 TCCTTCTGTGGACTTGACATTTTGAAGAACTCTTTCACAGATTAATGAGTTCATTTAG 660  
 605 TCCTTCTGTGGACTTGACATTTTGAAGAACTCTTTCACAGATTAATGAGTTCATTTAG 664  
 661 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 720  
 665 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 724  
 721 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 780  
 725 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 784  
 781 AGTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 840  
 785 AGTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 844  
 841 ATTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 900  
 845 ATTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 904  
 901 GAGTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 960  
 905 GAGTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 964  
 961 CCCCGGGTGGTGTAGAAAAGTATGTAATTTTCTGTTTAAAGACTTTGAACCTACC 1020  
 965 CCCCGGGTGGTGTAGAAAAGTATGTAATTTTCTGTTTAAAGACTTTGAACCTACC 1024  
 1021 TCAGAAGAGGAATCTAATACAAATTTTGAATTTTCCAGA 1062  
 1025 TCAGAAGAGGAATCTAATACAAATTTTGAATTTTCCAGA 1066

RESULT 5  
 AX015050  
 LOCUS AX015050 1088 bp DNA linear PAT 07-SEP-2000  
 DEFINITION Sequence 259 from Patent WO953040.  
 ACCESSION AX015050  
 VERSION AX015050.1 GI:10041189  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarczyk,C.  
 TITLE Human nucleic acid sequences from ovarian tumour tissue  
 JOURNAL Patent: WO 953040-A 259 21-OCT-1999;  
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BREND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)  
 FEATURES  
 source Location/Qualifiers  
 1. 1088  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT 302 a 216 c 254 g 316 t  
 ORIGIN

Query Match 82.3%; Score 1054.4; DB 6; Length 1088;  
 Best Local Similarity 99.9%; Fred. No. 3.9e-238;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAACATGGCGGCTCCACTAGGGGATGTTTCTGGGAGCACCACCCGGTCCCTCAGG 60  
 Db 5 CAAACATGGCGGCTCCACTAGGGGATGTTTCTGGGAGCACCACCCGGTCCCTCAGG 64

61 CCCGCGGGCTTCCGGGCCAAGCTTCGCTTCTTCAGGAGCTCCAGGGCTCTTAGAC 120  
 65 CCCGCGGGCTTCCGGGCCAAGCTTCGCTTCTTCAGGAGCTCCAGGGCTCTTAGAC 124  
 121 CTTCCAGCAGTACTTTGGTGGACGAGTTGGAGTCATCTTTCGAGGGCTTGGCTTGCATCTC 180  
 125 CTTCCAGCAGTACTTTGGTGGACGAGTTGGAGTCATCTTTCGAGGGCTTGGCTTGCATCTC 184  
 181 TGGTAGTCAAGACTATGTCAATGGCCACCGATCAGGAAGAAATTCGAACCGGTGTGATC 240  
 185 TGGTAGTCAAGACTATGTCAATGGCCACCGATCAGGAAGAAATTCGAACCGGTGTGATC 244  
 241 AGTGTATCCAGAGTTTCTGATATTCGAAGACAGACAGAAATTTTCTTACAAAAA 300  
 245 AGTGTATCCAGAGTTTCTGATATTCGAAGACAGACAGAAATTTTCTTACAAAAA 304  
 301 GATTGAGTTTCTGTCAGAAACAGAGCAAGTTATCAAGAGGATGTGTAGAACTAA 360  
 305 GATTGAGTTTCTGTCAGAAACAGAGCAAGTTATCAAGAGGATGTGTAGAACTAA 364  
 361 GGAATGAATACAGCGAAAGATGCACTAGTCCAGAGCACTTTGACAAAGCTGAGCAAT 420  
 365 GGAATGAATACAGCGAAAGATGCACTAGTCCAGAGCACTTTGACAAAGCTGAGCAAT 424  
 421 GGCAGAGGTCTCTGAGAGCAATCAACGTGAGCACAAAAAAGCCGCGACATCCCTCAGG 480  
 425 GGCAGAGGTCTCTGAGAGCAATCAACGTGAGCACAAAAAAGCCGCGACATCCCTCAGG 484  
 481 GCTCTTGGCTTCTGAGAGCAATCAACGTGAGCACAAAAAAGCCGCGACATCCCTCAGG 540  
 485 GCTCTTGGCTTCTGAGAGCAATCAACGTGAGCACAAAAAAGCCGCGACATCCCTCAGG 544  
 541 GAGCAAGGGCAGAGGAGGCTTGGCTATGAGTGGGCTGATGCGTGAAGTTGGCCACAT 600  
 545 GAGCAAGGGCAGAGGAGGCTTGGCTATGAGTGGGCTGATGCGTGAAGTTGGCCACAT 604  
 601 TCCTTCTGTGGACTTGACATTTTGGAGAACTCTTTGCCAGATATGAGTTCATTTTAG 660  
 605 TCCTTCTGTGGACTTGACATTTTGGAGAACTCTTTGCCAGATATGAGTTCATTTTAG 664  
 661 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 720  
 665 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 724  
 721 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 780  
 725 TTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 784  
 781 AGTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 840  
 785 AGTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 844  
 841 ATTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 900  
 845 ATTTTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 904  
 901 GAGTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 960  
 905 GAGTATGCTCCCATTTGAAATTTTCCACTATTTTATAAGCTGTAAATTTCTTGAGTAC 964  
 961 CCCCGGGTGGTGTAGAAAAGTATGTAATTTTCTGTTTAAAGACTTTGAACCTACC 1020  
 965 CCCCGGGTGGTGTAGAAAAGTATGTAATTTTCTGTTTAAAGACTTTGAACCTACC 1024  
 1021 TCAGAAGAGGAATCTAATACAAATTTTGAATTTTCCAGA 1056  
 1025 TCAGAAGAGGAATCTAATACAAATTTTGAATTTTCCAGA 1060

RESULT 6  
 BC011936  
 LOCUS BC011936 1083 bp mRNA linear PRI 02-AUG-2001

```

/mol_type="mRNA"
/db_xref="taxon:9606"
1759..2295
/codon_start=1
/product="unknown"
/protein_id="AAG38612.1"
/db_xref="GI:11596418"
/translation="MAAPLGMFSGPPGPAPGLPQASLLQAAFGAPRPSSTL
VDELFSEAFACFASLUSODVNGTDOEEIRTVGDCIOKPLDIARQETCFLOKRLQ
SVKPBQVIFEDVSELNELQKDALVQKHLTKLHMQVLESDINVQHKPADIPQGS
LAYDEQASNIPAPLPT"
BASE COUNT 980 a 503 c 621 g 1005 t
ORIGIN

Query Match 100.0%; Score 1281; DB 9; Length 3109;
Best Local Similarity 100.0%; Pred. No. 1.4e-291;
Matches 1281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACATGGCGCTCCACTAGGGGGTATGTTTCTGGGAGCCACCCGGTCCCTCAGG 60
DB 1754 CAACATGGCGCTCCACTAGGGGGTATGTTTCTGGGAGCCACCCGGTCCCTCAGG 1813
QY 61 CCCGCGGGCTTCCGGGCAAGCTTCGCTTCTCAGGCAGCTCCAGGCGTCTAGAC 120
DB 1814 CCCGCGGGCTTCCGGGCAAGCTTCGCTTCTCAGGCAGCTCCAGGCGTCTAGAC 1873
QY 121 CTTCCAGCAGTACTTGGTGGAGCGAGTTGGAGTCACTTTTCAGGCGTCTGTTGATCTC 180
DB 1874 CTTCCAGCAGTACTTGGTGGAGCGAGTTGGAGTCACTTTTCAGGCGTCTGTTGATCTC 1933
QY 181 TGGTGGTCCAGGCTATGTCATGGCCAGCATCAGGAGAAATCCAGCGGTGTGATC 240
DB 1934 TGGTGGTCCAGGCTATGTCATGGCCAGCATCAGGAGAAATCCAGCGGTGTGATC 1993
QY 241 AGTGTATCCAGAGTTTCTGGATATTCAGACAGACAGAAATGTTTCTTACAAAAA 300
DB 1994 AGTGTATCCAGAGTTTCTGGATATTCAGACAGACAGAAATGTTTCTTACAAAAA 2053
QY 301 GATTGCACTTATCTCCAGAAACAGGCAAGTTATCAAGAGGAGTGTTCAGACATTA 360
DB 2054 GATTGCACTTATCTCCAGAAACAGGCAAGTTATCAAGAGGAGTGTTCAGACATTA 2113
QY 361 GGAATGAATACAGCGGAAAGATCAGTCCAGAGACATCTTGACAAAGCTGAGGCATT 420
DB 2114 GGAATGAATACAGCGGAAAGATCAGTCCAGAGACATCTTGACAAAGCTGAGGCATT 2173
QY 421 GCGACAGTCTCGAGGACATCAAGCTGAGCAGCAAAAGCCGCGACATCCCTCAGG 480
DB 2174 GCGACAGTCTCGAGGACATCAAGCTGAGCAGCAAAAGCCGCGACATCCCTCAGG 2233
QY 481 GTCCTTGGCTTACTGGAGCAGCATCTGCAACATCCCTGCACCTCTGAAGCCAACT 540
DB 2234 GTCCTTGGCTTACTGGAGCAGCATCTGCAACATCCCTGCACCTCTGAAGCCAACT 2293
QY 541 GAGCAAGGCGAGGAGGAGTGGCTATGATGGGCTGATCGGTGAGTGGCCACAT 600
DB 2294 GAGCAAGGCGAGGAGGAGTGGGCTATGATGGGCTGATCGGTGAGTGGCCACAT 2353
QY 601 TCCTTCTGTGGACTTGACATTTTGGAGAACTCTTTGCCAGATAATGAGTTCATTTAG 660
DB 2354 TCCTTCTGTGGACTTGACATTTTGGAGAACTCTTTGCCAGATAATGAGTTCATTTAG 2413
QY 661 TTTTATGCTCCATGAAATTTTCCACTATTTTATAGCTGTTAAATTTCTTGAGTAC 720
DB 2414 TTTTATGCTCCATGAAATTTTCCACTATTTTATAGCTGTTAAATTTCTTGAGTAC 2473
QY 721 TTTTAAACATGCTGTAGCTTGGATTAACCAAGTAAGTATTTTCTTTAGCAA 780
DB 2474 TTTTAAACATGCTGTAGCTTGGATTAACCAAGTAAGTATTTTCTTTAGCAA 2533
QY 781 AGTTAGACTGGAATATGATGACACAGATCTTTTATAGTGGCTGCTGTTTAA 840
DB 2534 AGTTAGACTGGAATATGATGACACAGATCTTTTATAGTGGCTGCTGTTTAA 2593

```

```

QY 841 ATTTTGCATGACTTTTCATCTTTTATATGTTGTTTCTCTAGTTTGCAGGAAAA 900
DB 2594 ATTTTGCATGACTTTTCATCTTTTATATGTTGTTTCTCTAGTTTGCAGGAAAA 2653
QY 901 GAGTATAGTAGCTCAGAAATCAGGAGATGGAGTCTTTAGTCGTAGGCTTATGATTA 960
DB 2654 GAGTATAGTAGCTCAGAAATCAGGAGATGGAGTCTTTAGTCGTAGGCTTATGATTA 2713
QY 961 CCCCGGGTGGTGTAGAAAAGTATGTAATTTGCTCTGTTTAAAGACTTTGACATACC 1620
DB 2714 CCCCGGGTGGTGTAGAAAAGTATGTAATTTGCTCTGTTTAAAGACTTTGACATACC 2773
QY 1021 TCAAGAAGAGGAATCTAATACAATATTTGTAATGTTTCCAGAGCTCTCAGAAAGGATT 1080
DB 2774 TCAAGAAGAGGAATCTAATACAATATTTGTAATGTTTCCAGAGCTCTCAGAAAGGATT 2833
QY 1081 TTTTGTAAATAGTCAGAGACGATGGAACTGCTCGGGTATAGTATAGTAACTTACAG 1140
DB 2834 TTTTGTAAATAGTCAGAGACGATGGAACTGCTCGGGTATAGTATAGTAACTTACAG 2893
QY 1141 TAGGATCCCTAGTGTGATGCTGACTTCTGTTGGGTATGTTATATTTATGTTGTT 1200
DB 2894 TAGGATCCCTAGTGTGATGCTGACTTCTGTTGGGTATGTTATATTTATGTTGTT 2953
QY 1201 TACTTTTTTTTTCACATAAAGATATAGTGGAGCAGTACGCTAACATTCATTA 1260
DB 2954 TACTTTTTTTTTCACATAAAGATATAGTGGAGCAGTACGCTAACATTCATTA 3013
QY 1261 CATTTCTGCAAGTAATGAATCTG 1281
DB 3014 CATTTCTGCAAGTAATGAATCTG 3034

RESULT 3
AX017517
LOCUS AX017517 1071 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 65 from Patent WO9947655.
ACCESSION AX017517
VERSION AX017517.1 GI:10042314
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pillarsky,C.
TITLE Human nucleic acid sequences from normal breast tissue
JOURNAL Patent: WO 9947655-A 65 23-SEP-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILLARSKY CHRISTIAN (DE)
FEATURES
source 1..1071
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 281 a 218 c 255 g 317 t
ORIGIN

Query Match 82.8%; Score 1060.4; DB 6; Length 1071;
Best Local Similarity 99.9%; Pred. No. 1.5e-239;
Matches 1061; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAACATGGCGGCTCCACTAGGGGGTATGTTTCTGGGAGCCACCCGGTCCCTCAGG 60
DB 5 CAAACATGGCGGCTCCACTAGGGGGTATGTTTCTGGGAGCCACCCGGTCCCTCAGG 64
QY 61 CCCCGCGGGGCTTCCGGGCAAGCTTCGCTTCTTTCAGGAGCTCCAGGCGCTCTAGAC 120
DB 65 CCCCGCGGGGCTTCCGGGCAAGCTTCGCTTCTTTCAGGAGCTCCAGGCGCTCTAGAC 124

```

CDS

121	QY	CTTCAGCAGTACTTTGGTGGACGAGTTGAGTCACTTTTCGAGCGTTGCTTTGCATCTC	180
122	DB		
123	DB	CTTCAGCAGTACTTTGGTGGACGAGTTGAGTCACTTTTCGAGCGTTGCTTTGCATCTC	184
124	DB		
181	QY	TGGTGAGTCAGCACTATGTCAATGGCACCGATCAGGAAGAAATTCGAACCGGTGTTGATC	240
182	DB		
183	DB	TGGTGAGTCAGCACTATGTCAATGGCACCGATCAGGAAGAAATTCGAACCGGTGTTGATC	244
184	DB		
241	QY	AGTGATCCAGAACTTTCTGGATATTGCAAGACAGACAGATGTTTTTTCTTACAAAAA	300
242	DB		
243	DB	AGTGATCCAGAACTTTCTGGATATTGCAAGACAGACAGATGTTTTTTCTTACAAAAA	304
244	DB		
301	QY	GATTGCAGTTATCTGTCCAGAAACACAGAGCAAGTTATCAAGAGAGATGTGTCAAGACTAA	360
302	DB		
303	DB	GATTGCAGTTATCTGTCCAGAAACACAGAGCAAGTTATCAAGAGAGATGTGTCAAGACTAA	364
304	DB		
361	QY	GGATGAATTACAGCGGGAAGATGCACTAGTCCAGAGACACTTGCACAGCTGAGGCATT	420
362	DB		
363	DB	GGATGAATTACAGCGGGAAGATGCACTAGTCCAGAGACACTTGCACAGCTGAGGCATT	424
364	DB		
421	QY	GGCAGCAGGTGCTGGAGGACATCAACGTGCAGACAAAAAGCCGCGACATCCCTCAGG	480
422	DB		
423	DB	GGCAGCAGGTGCTGGAGGACATCAACGTGCAGACAAAAAGCCGCGACATCCCTCAGG	484
424	DB		
481	QY	GCTCCTTGGCCCTACTCTGAGCAGGCACTCTGCCAACATCCCTGCACCTCTCGAAGCCCAAGT	540
482	DB		
483	DB	GCTCCTTGGCCCTACTCTGAGCAGGCACTCTGCCAACATCCCTGCACCTCTCGAAGCCCAAGT	544
484	DB		
541	QY	GAGCAAAAGGGCAGAGGCAAGTTGBCCTATGATGGGCTGATGGCTGAGGTGGCCACACAT	600
542	DB		
543	DB	GAGCAAAAGGGCAGAGGCAAGTTGBCCTATGATGGGCTGATGGCTGAGGTGGCCACACAT	604
544	DB		
601	QY	TCCCTCCCTGTGCGACTTGCACATTTTGGAAAGAACTCTTTGCCAGATAATCAGTTTCATTTTAG	660
602	DB		
603	DB	TCCCTCCCTGTGCGACTTGCACATTTTGGAAAGAACTCTTTGCCAGATAATCAGTTTCATTTTAG	664
604	DB		
661	QY	TTTTATGCTCCATTTGAAGAAATTTCCACTATTTTATTAAGCTGTAAATCTCTGAGTAC	720
662	DB		
663	DB	TTTTATGCTCCATTTGAAGAAATTTCCACTATTTTATTAAGCTGTAAATCTCTGAGTAC	724
664	DB		
721	QY	TTTTAACAATGCTGTAGCTTGGATAAACCAAGTAAGTATTTTTTTTGTCTTTAGCAA	780
722	DB		
723	DB	TTTTAACAATGCTGTAGCTTGGATAAACCAAGTAAGTATTTTTTTTGTCTTTAGCAA	784
724	DB		
781	QY	AGTTTAGACTCGTAATATGATGACACAGATCTTTTATAGTGGCTTTGCTGTTTAA	840
782	DB		
783	DB	AGTTTAGACTCGTAATATGATGACACAGATCTTTTATAGTGGCTTTGCTGTTTAA	844
784	DB		
841	QY	ATTTTGTGACCTTTTCATCTTTTATATGTGTTTCTGTATGTTTGATCCGAAGGAAAA	900
842	DB		
843	DB	ATTTTGTGACCTTTTCATCTTTTATATGTGTTTCTGTATGTTTGATCCGAAGGAAAA	904
844	DB		
901	QY	GAGTATAGTAGCCTGAGAAATCAGAGATGGGAGTTTTAGTCGTAGGCCCTTATGATAATTA	960
902	DB		
903	DB	GAGTATAGTAGCCTGAGAAATCAGAGATGGGAGTTTTAGTCGTAGGCCCTTATGATAATTA	964
904	DB		
961	QY	CCCCGGGTGGTGTAGAAAAAGTATGTAATTTGCTGTTTTAAGCACTTGAACCTACC	1020
962	DB		
963	DB	CCCCGGGTGGTGTAGAAAAAGTATGTAATTTGCTGTTTTAAGCACTTGAACCTACC	1024
964	DB		
1021	QY	TCAGAAGAGGAATCTAAATACAAATTTGTAATGTTTCCAGA	1062
1022	DB		
1023	DB	TCAGAAGAGGAATCTAAATACAAATTTGTAATGTTTCCAGA	1066
1024	DB		

SULT 4	1071 bp	DNA	linear	PAT 1a-SEP-2002
335207	Human nucleic acid sequence originating in normal mammary tissue.			
CUS	BD135207			
FINITION	BD135207			
SSION	BD135207.1			
SSION	GI:232330152			
WORDSD	JP 2002506639-A/54.			
FORCE	Homo sapiens (human)			

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Speft, T., Hintzman, B., Shcmitt, A., Pitaraki, C., Duhl, E. and Rosenthal, A.
TITLE	Human nucleic acid sequence originating in normal mammary tissue
JOURNAL	Patent: JP 2002506639-A 54 05-MAR-2002;
COMMENT	METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH OS Homo sapiens (human) PN JP 2002506639-A/54 PD 05-MAR-2002 PF 19-MAR-1999 JP 2000536838 PR 20-MAR-1998 DE 198 13 835.0 PI THOMAS SPEFT, BERND HINTZMAN, ARMIN SHCMITT, CHRISTIAN PIRARSKI, PI EDGAR DUHL, PI ANDRE ROSENTHAL PC C12N15/09, A61K48/00, A61P35/00, A61P43/00, A61P43/00, C07K14/47, PC C07K16/18, PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//A61K38/00, PC C12N15/00, PC C12N5/00, A61K37/02 CC Human nucleic acid sequence originating in normal mammary CC tissue
PH Key	Location/Qualifiers
FT source	1..1071 /organism='Homo sapiens (human)'
FEATURES	Location/Qualifiers
source	1..1071 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'
BASE COUNT	281 a 218 c 255 g 317 t
ORIGIN	
Query Match	82.8%; Score 1060.4; DB 6; Length 1071;
Best Local Similarity	99.9%; Pred. No. 1.5e-239;
Matches 1061; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
Qy	1 CAAACATGGCGCTCCACTAGGGGGTATGTTTTCTGGCAGCCACCCGGTCCCTCAGG 60
Db	5 CAACATGGCGCTCCACTAGGGGGTATGTTTTCTGGCAGCCACCCGGTCCCTCAGG 64
Qy	61 CCGCGCGGGCCCTCCGGGCCAAGCTTCGCTTCCTCAGGAGCTCAGGGCTCTAGAC 120
Db	65 CCGCGCGGGCCCTCCGGGCCAAGCTTCGCTTCCTCAGGAGCTCAGGGCTCTAGAC 124
Qy	121 CTTCCAGCAGTACTTTGGTGGACAGTGGAGTCACTTTTCGAGGCTTGCTTTGCATCTC 180
Db	125 CTTCCAGCAGTACTTTGGTGGACAGTGGAGTCACTTTTCGAGGCTTGCTTTGCATCTC 184
Qy	181 TGGTGAGTCCAGACTATGTCATCGCACCGCATCAGGAAGAAATTCGAACCGGTGTGATC 240
Db	185 TGGTGAGTCCAGACTATGTCATCGCACCGCATCAGGAAGAAATTCGAACCGGTGTGATC 244
Qy	241 AGTGTATCCAGAAGTTCTCGATATTGCAAGACAGACAGAAATGTTTTCTTACAAAAA 300
Db	245 AGTGTATCCAGAAGTTCTCGATATTGCAAGACAGACAGAAATGTTTTCTTACAAAAA 304
Qy	301 GATTCGAGTTATCTGTCCAGAAACACGACGACAGTTATCAAGAGGAGTGTCTCAGACTAA 360
Db	305 GATTCGAGTTATCTGTCCAGAAACACGACGACAGTTATCAAGAGGAGTGTCTCAGACTAA 364
Qy	361 GGAATGAATTACAGCGGAAAGATGCACTAGTCCAGAGCACTTTGACAAAGCTGAGGCATT 420
Db	365 GGAATGAATTACAGCGGAAAGATGCACTAGTCCAGAGCACTTTGACAAAGCTGAGGCATT 424
Qy	421 GGCAGCAGTGTCTGGAGGACATCAACGTGCAGACAAAAAGCCCGCCGACATCCCTCAGG 480
Db	425 GGCAGCAGTGTCTGGAGGACATCAACGTGCAGACAAAAAGCCCGCCGACATCCCTCAGG 484
Qy	481 GTCTCTTGGCTTACTTGGAGCGGCACTCTGCCAACATCTCCCTGCACCTCTGAAAGCCAACT 540